UNITED STATES PATENT AND TRADEMARK OFFICE

APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
09/425,804	10/25/1999	DAVID G. GORENSTEIN	122144-1001	1041

7590   12/06/2001

Gardere Wynne Sewell LLP
Sanford E. Warren, Jr.
3000 Thanksgiving Tower
1601 Elm Street
DALLAS, TX 75201-4761

EXAMINER
BHATTI, TAHIRA H

ART UNIT	PAPER NUMBER
1627	12

DATE MAILED: 12/06/2001

Please find below and/or attached an Office communication concerning this application or proceeding.

PTO-90C (Rev. 07-01)

UNITED STATES DEPARTMENT OF COMMERCE
Patent and Trademark Office
COMMISSIONER OF PATENTS AND TRADEMARKS
Washington, D.C. 20231

SERIAL NUMBER	FILING DATE	FIRST NAMED APPLICANT	ATTORNEY DOCKET NO.
09/425,804			

EXAMINER

ART UNIT	PAPER NUMBER
1627	12

Please find below a communication from the EXAMINER in charge of this application

Sequence Rules: Bonafide Attempt Letter

The forwarded Sequence Letter e.g. "Notice to Comply with Sequence Rules" dated 10/1/01 in paper no. 10 is hereby vacated in light of the "Raw Sequence Listing Error Report" received by the Examiner on 10/5/01 (paper no. 11) a copy of which is enclosed herewith.

This application contains sequence disclosures that are encompassed by the definitions for nucleotide and/or amino acid sequences set forth in 37 CFR 1.821(a)(1) and (a)(2); but fails to comply with the requirements of 37 CFR 1.821 through 1.825 for the reason(s) set forth on the attached "Raw Sequence Listing Error Report". Applicant must comply with the requirements of the sequence rules (37 CFR 1.821 - 1.825) before the application can be examined under 35 U.S.C. §§ 131 and 132. Applicant must comply with the requirements of the sequence rules (37 CFR 1.821 - 1.825) before the application can be further examined.

Since the above-mentioned reply appears to be *bona fide* attempt to comply with the requirements of the sequence rules (37 CFR 1.821 - 1.825), applicant is given a TIME PERIOD of **ONE (1) MONTH** from the mailing date of this communication within which to correct the deficiency so as to comply with the sequence rules (37 CFR 1.821 - 1.825) in order to avoid abandonment of the application under 37 CFR 1.821(g). EXTENSIONS OF THIS TIME PERIOD MAY BE GRANTED UNDER 37 CFR 1.136(a).

General information regarding further correspondence

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Examiner Celsa whose telephone number is (703) 305-7556.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Jyothsna Venkat (art unit 1627), can be reached at (703)308-0570.

Any inquiry of a general nature, or relating to the status of this application, should be directed to the Group receptionist whose telephone number is (703) 308-0196.

Tahira Bhatti (art unit 1627)
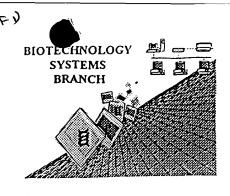
December 3, 2001

BENNETT CELSA
PRIMARY EXAMINER

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 CFR 1.821 - 1.825 for the following reason(s):

☒ 1. This application clearly fails to comply with the requirements of 37 CFR 1.821 - 1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.

☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 CFR 1.821(c).

☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 CFR 1.821(

☒ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 CFR 1.822 and/or 1.823, as indicated on the attached marked-up copy of the "Raw Sequence Listing."

☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A substitute computer readable form must be submitted as required by 37 CFR 1.825(d).

☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 CFR 1.821(e).

☐ 7. Other: _____

Applicant must provide:

☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing"

☒ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification

☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 CFR 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d)

For questions regarding compliance with these requirements, please contact:

For Rules Interpretation, call (703) 308-1123
For CRF submission help, call (703) 308-4212
For PatentIn software help, call (703) 308-6856

Please return a copy of this notice with your response.

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/425,804

RECEIVED

Source: 1623

OCT 0 5 2001

Date Processed by STIC: 9/27/2001

TECH CENTER 1600/2900

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER VERSION 3.0 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).
Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

<u>Checker Version 3.0 can be down loaded from the USPTO website at the following address:</u>
http://www.uspto.gov/web/offices/pac/checker

Raw Sequence Listing Error Summary

ERROR DETECTED **SUGGESTED CORRECTION** SERIAL NUMBER: 09/425,804.

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1____Wrapped Nucleics   The number/text at the end of each line "wrapped" down to the next line. This may occur if your file
    Wrapped Aminos   was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will
                prevent "wrapping."

2____Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.

3____Misaligned Amino   The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers;
    Numbering   use space characters, instead.

4____Non-ASCII   The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please
                ensure your subsequent submission is saved in ASCII text.

5____Variable Length   Sequence(s)____contain n's or Xaa's representing more than one residue. Per Sequence Rules,
                each n or Xaa can only represent a single residue. Please present the maximum number of each
                residue having variable length and indicate in the <220>-<223> section that some may be missing.

6____PatentIn 2.0   A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
    "bug"   sequences(s) _____. Normally, PatentIn would automatically generate this section from the
                previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to
                the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for
                Artificial or Unknown sequences.

7____Skipped Sequences Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
    (OLD RULES)   (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
                (i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
                (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
                This sequence is intentionally skipped

                Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8____Skipped Sequences Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
    (NEW RULES)   <210> sequence id number
                <400> sequence id number
                000

9____Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing.
    (NEW RULES)   Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
                In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10____Invalid <213>   Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or
    Response   scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or
                is Artificial Sequence

11____Use of <220>   Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.
                Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or
                "Unknown." Please explain source of genetic material in <220> to <223> section.
                (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12____PatentIn 2.0   Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,
    "bug"   resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence
                listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

AMC – Biotechnology Systems Branch – 06/04/2001

1623

RAW SEQUENCE LISTING   DATE: 09/27/2001
PATENT APPLICATION: US/09/425,804   TIME: 11:23:40

Input Set : **A:\Nfkbapt1.app**
Output Set: **N:\CRF3\09272001\I425804.raw**

```
 3 <110> APPLICANT: Gorenstein, David G.
 4        King, David J.
 5        Ventura, Daniel A.
 6        Brasier, Allan R.
 8 <120> TITLE OF INVENTION: Thio-Modified Aptamer Synthetic Methods and
 9        Compositions
11 <130> FILE REFERENCE: 122144-002000
```
C--> `13 <140> CURRENT APPLICATION NUMBER: US/09/425,804`
C--> `14 <141> CURRENT FILING DATE: 1999-10-25`
```
16 <150> PRIOR APPLICATION NUMBER: 60/105,600
17 <151> PRIOR FILING DATE: 1998-10-26
19 <160> NUMBER OF SEQ ID NOS: 50
21 <170> SOFTWARE: PatentIn Ver. 2.1
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 66
25 <212> TYPE: DNA
26 <213> ORGANISM: Artificial Sequence
28 <220> FEATURE:
29 <223> OTHER INFORMATION: Description of Artificial Sequence: aptamer
31 <400> SEQUENCE: 1
```
W--> `32 cagtgctcta gaggatccgt gacnnnnnnn nnnnnnnnnn nnnnncgaag cttatcgatc 60`
```
33 cgagcg                                                             66
36 <210> SEQ ID NO: 2
37 <211> LENGTH: 22
38 <212> TYPE: DNA
39 <213> ORGANISM: Artificial Sequence
41 <220> FEATURE:
42 <223> OTHER INFORMATION: Description of Artificial Sequence: aptamer
44 <400> SEQUENCE: 2
45 gccgtccaca tacgacacca cc                                           22
48 <210> SEQ ID NO: 3
49 <211> LENGTH: 22
50 <212> TYPE: DNA
51 <213> ORGANISM: Artificial Sequence
53 <220> FEATURE:
54 <223> OTHER INFORMATION: Description of Artificial Sequence: aptamer
56 <400> SEQUENCE: 3
57 ggccgaccgc acagcacaac cc                                           22
60 <210> SEQ ID NO: 4
61 <211> LENGTH: 22
62 <212> TYPE: DNA
63 <213> ORGANISM: Artificial Sequence
65 <220> FEATURE:
66 <223> OTHER INFORMATION: Description of Artificial Sequence: aptamer
68 <400> SEQUENCE: 4
69 ggcgcggata caacccacac gc                                           22
72 <210> SEQ ID NO: 5
```

Does Not Comply
Corrected Diskette Needed

See item # 9 on
ERROR summary
sheet.

RAW SEQUENCE LISTING   DATE: 09/27/2001
PATENT APPLICATION: US/09/425,804   TIME: 11:23:40

Input Set : A:\Nfkbapt1.app
Output Set: N:\CRF3\09272001\I425804.raw

```
73  <211> LENGTH: 22
74  <212> TYPE: DNA
75  <213> ORGANISM: Artificial Sequence
77  <220> FEATURE:
78  <223> OTHER INFORMATION: Description of Artificial Sequence: aptamer
80  <400> SEQUENCE: 5
81  gggcccgctg tacatgcaca cg                                      22
84  <210> SEQ ID NO: 6
85  <211> LENGTH: 22
86  <212> TYPE: DNA
87  <213> ORGANISM: Artificial Sequence
89  <220> FEATURE:
90  <223> OTHER INFORMATION: Description of Artificial Sequence: aptamer
92  <400> SEQUENCE: 6
93  ggccgaccgc acagcacaac cc                                      22
96  <210> SEQ ID NO: 7
97  <211> LENGTH: 22
98  <212> TYPE: DNA
99  <213> ORGANISM: Artificial Sequence
101 <220> FEATURE:
102 <223> OTHER INFORMATION: Description of Artificial Sequence: aptamer
104 <400> SEQUENCE: 7
105 gggcccgctg tacatgcaca cg                                      22
108 <210> SEQ ID NO: 8
109 <211> LENGTH: 22
110 <212> TYPE: DNA
111 <213> ORGANISM: Artificial Sequence
113 <220> FEATURE:
114 <223> OTHER INFORMATION: Description of Artificial Sequence: aptamer
116 <400> SEQUENCE: 8
117 gggcccgctg cacgtgcaca cg                                      22
120 <210> SEQ ID NO: 9
121 <211> LENGTH: 22
122 <212> TYPE: DNA
123 <213> ORGANISM: Artificial Sequence
125 <220> FEATURE:
126 <223> OTHER INFORMATION: Description of Artificial Sequence: aptamer
128 <400> SEQUENCE: 9
129 gggcccgctg tacacgcaca cg                                      22
132 <210> SEQ ID NO: 10
133 <211> LENGTH: 22
134 <212> TYPE: DNA
135 <213> ORGANISM: Artificial Sequence
137 <220> FEATURE:
138 <223> OTHER INFORMATION: Description of Artificial Sequence: aptamer
140 <400> SEQUENCE: 10
141 cccgttgttg tcccactcca cg                                      22
144 <210> SEQ ID NO: 11
145 <211> LENGTH: 22
```

RAW SEQUENCE LISTING   DATE: 09/27/2001
PATENT APPLICATION: US/09/425,804   TIME: 11:23:40

Input Set : A:\Nfkbapt1.app
Output Set: N:\CRF3\09272001\I425804.raw

```
146 <212> TYPE: DNA
147 <213> ORGANISM: Artificial Sequence
149 <220> FEATURE:
150 <223> OTHER INFORMATION: Description of Artificial Sequence: aptamer
152 <400> SEQUENCE: 11
153 cccgttgttg tcccgctcca cg                                     22
156 <210> SEQ ID NO: 12
157 <211> LENGTH: 10
158 <212> TYPE: DNA
159 <213> ORGANISM: Artificial Sequence
161 <220> FEATURE:
162 <223> OTHER INFORMATION: Description of Artificial Sequence: aptamer
164 <400> SEQUENCE: 12
165 gttgcgcaac                                                    10
168 <210> SEQ ID NO: 13
169 <211> LENGTH: 10
170 <212> TYPE: DNA
171 <213> ORGANISM: Artificial Sequence
173 <220> FEATURE:
174 <223> OTHER INFORMATION: Description of Artificial Sequence: aptamer
176 <400> SEQUENCE: 13
177 gctgtacatg                                                    10
180 <210> SEQ ID NO: 14
181 <211> LENGTH: 10
182 <212> TYPE: DNA
183 <213> ORGANISM: Artificial Sequence
185 <220> FEATURE:
186 <223> OTHER INFORMATION: Description of Artificial Sequence: aptamer
188 <400> SEQUENCE: 14
189 gttgtcccac                                                    10
192 <210> SEQ ID NO: 15
193 <211> LENGTH: 10
194 <212> TYPE: DNA
195 <213> ORGANISM: Artificial Sequence
197 <220> FEATURE:
198 <223> OTHER INFORMATION: Description of Artificial Sequence: aptamer
200 <400> SEQUENCE: 15
201 gttgttgtcc                                                    10
204 <210> SEQ ID NO: 16
205 <211> LENGTH: 20
206 <212> TYPE: DNA
207 <213> ORGANISM: Artificial Sequence
209 <220> FEATURE:
210 <223> OTHER INFORMATION: Description of Artificial Sequence: aptamer
212 <400> SEQUENCE: 16
213 tgcagattgc gcaatctgca                                         20
216 <210> SEQ ID NO: 17
217 <211> LENGTH: 22
218 <212> TYPE: DNA
```

RAW SEQUENCE LISTING   DATE: 09/27/2001
PATENT APPLICATION: US/09/425,804   TIME: 11:23:40

Input Set : A:\Nfkbapt1.app
Output Set: N:\CRF3\09272001\I425804.raw

```
219 <213> ORGANISM: Artificial Sequence
221 <220> FEATURE:
222 <223> OTHER INFORMATION: Description of Artificial Sequence: aptamer
224 <400> SEQUENCE: 17
225 cgtgtgcatg tacagcgggc cc                                        22
228 <210> SEQ ID NO: 18
229 <211> LENGTH: 42
230 <212> TYPE: DNA
231 <213> ORGANISM: Artificial Sequence
233 <220> FEATURE:
234 <223> OTHER INFORMATION: Description of Artificial Sequence: aptamer
236 <400> SEQUENCE: 18
237 ccaggagatt ccacccagga gattccaccc aggagattcc ac                  42
240 <210> SEQ ID NO: 19
241 <211> LENGTH: 14
242 <212> TYPE: DNA
243 <213> ORGANISM: Artificial Sequence
245 <220> FEATURE:
246 <223> OTHER INFORMATION: Description of Artificial Sequence: aptamer
248 <400> SEQUENCE: 19
249 ccaggagatt ccac                                                 14
252 <210> SEQ ID NO: 20
253 <211> LENGTH: 10
254 <212> TYPE: DNA
255 <213> ORGANISM: Artificial Sequence
257 <220> FEATURE:
258 <223> OTHER INFORMATION: Description of Artificial Sequence: aptamer
260 <400> SEQUENCE: 20
261 ggggacttcc                                                      10
264 <210> SEQ ID NO: 21
265 <211> LENGTH: 62
266 <212> TYPE: DNA                            see page 1
267 <213> ORGANISM: Artificial Sequence
269 <220> FEATURE:
270 <223> OTHER INFORMATION: Description of Artificial Sequence: aptamer
272 <400> SEQUENCE: 21
W--> 273 atgcttccac gagcctttcn nnnnnnnnnn nnnnnnnnnn nctgcgaggc ggtagtctat 60
274 tc                                                              62
277 <210> SEQ ID NO: 22
278 <211> LENGTH: 22
279 <212> TYPE: DNA
280 <213> ORGANISM: Artificial Sequence
282 <220> FEATURE:
283 <223> OTHER INFORMATION: Description of Artificial Sequence: aptamer
285 <400> SEQUENCE: 22
286 ggggcggggg gatatggaca cc                                        22
289 <210> SEQ ID NO: 23
290 <211> LENGTH: 22
291 <212> TYPE: DNA
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RAW SEQUENCE LISTING   DATE: 09/27/2001
PATENT APPLICATION: **US/09/425,804**   TIME: 11:23:40

Input Set : **A:\Nfkbapt1.app**
Output Set: **N:\CRF3\09272001\I425804.raw**

```
292 <213> ORGANISM: Artificial Sequence
294 <220> FEATURE:
295 <223> OTHER INFORMATION: Description of Artificial Sequence: aptamer
297 <400> SEQUENCE: 23
298 gggctggtgt ggtagactcc cc                                          22
301 <210> SEQ ID NO: 24
302 <211> LENGTH: 22
303 <212> TYPE: DNA
304 <213> ORGANISM: Artificial Sequence
306 <220> FEATURE:
307 <223> OTHER INFORMATION: Description of Artificial Sequence: aptamer
309 <400> SEQUENCE: 24
310 cccgcccaca cacaccgccc cc                                          22
313 <210> SEQ ID NO: 25
314 <211> LENGTH: 23
315 <212> TYPE: DNA
316 <213> ORGANISM: Artificial Sequence
318 <220> FEATURE:
319 <223> OTHER INFORMATION: Description of Artificial Sequence: aptamer
321 <400> SEQUENCE: 25
322 gggccgggag agaacatagc gac                                         23
325 <210> SEQ ID NO: 26
326 <211> LENGTH: 22
327 <212> TYPE: DNA
328 <213> ORGANISM: Artificial Sequence
330 <220> FEATURE:
331 <223> OTHER INFORMATION: Description of Artificial Sequence: aptamer
333 <400> SEQUENCE: 26
```
W--> `334 cccnnnnca cacaccgccc cc`   *See page 1*   `22`
```
337 <210> SEQ ID NO: 27
338 <211> LENGTH: 22
339 <212> TYPE: DNA
340 <213> ORGANISM: Artificial Sequence
342 <220> FEATURE:
343 <223> OTHER INFORMATION: Description of Artificial Sequence: aptamer
345 <400> SEQUENCE: 27
346 ggtatactct ccgcccctcc cc                                          22
349 <210> SEQ ID NO: 28
350 <211> LENGTH: 26
351 <212> TYPE: DNA
352 <213> ORGANISM: Artificial Sequence
354 <220> FEATURE:
355 <223> OTHER INFORMATION: Description of Artificial Sequence: aptamer
357 <400> SEQUENCE: 28
358 cccacatgta cacgccgccc ccgccc                                      26
361 <210> SEQ ID NO: 29
362 <211> LENGTH: 22
363 <212> TYPE: DNA
364 <213> ORGANISM: Artificial Sequence
```

FYI.

Use of n and/or Xaa has been detected in the
Sequence Listing. Review the Sequence Listing
to ensure a corresponding explanation is present
in the <220> to <223> fields of each sequence
using n or Xaa.

VERIFICATION SUMMARY   DATE: 09/27/2001
PATENT APPLICATION: **US/09/425,804**   TIME: 11:23:41

Input Set : **A:\Nfkbaptl.app**
Output Set: **N:\CRF3\09272001\I425804.raw**

```
L:13 M:270 C: Current Application Number differs, Replaced Current Application Number
L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:32 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:1
L:32 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:1
L:32 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:273 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:21
L:273 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:21
L:273 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:334 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:26
L:334 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:26
L:334 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26
L:370 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:29
L:370 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:29
L:370 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29
```